

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 23, 1999, 23:01:43 ; Search time 360.53 Seconds
(without alignments)
621.966 Million cell updates/sec

Title: US-09-205-015-2
Perfect score: 147
Sequence: 1 agataactgggcaaccatg.....ctcccccctctgttatct 147

Scoring table: IDENTITY_NUC

Searched: 2002476 seqs, 762712212 residues

Database : EST:*

1: em_est1:.*
2: em_est2:.*
3: em_est3:.*
4: em_est4:.*
5: em_est5:.*
6: em_est6:.*
7: em_est7:.*
8: em_est8:.*
9: em_est9:.*
10: gb_est1:.*
11: gb_est2:.*
12: gb_est3:.*
13: gb_est4:.*
14: gb_est5:.*
15: gb_est6:.*
16: gb_est7:.*
17: gb_est8:.*
18: gb_est9:.*
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22: gb_est13:.*
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25: gb_est16:.*
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27: gb_est18:.*
28: gb_est19:.*
29: gb_est20:.*
30: gb_est21:.*
31: gb_est22:.*
32: em_est10:.*
33: em_est11:.*
34: em_est12:.*
35: em_est13:.*
36: em_est14:.*
37: em_est15:.*
38: em_est16:.*
39: em_est17:.*
40: em_est18:.*
41: em_est19:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33.2	22.6	443	17	F19640 H.sapiens E
2	30.6	20.8	447	24	AA646832 vn37d04.r

C	3	30.4	20.7	381	11	H51183
C	4	29.8	20.3	447	11	R87592
	5	29.4	20.0	363	28	AA893137
	6	29.2	19.9	539	10	R18712
	7	29.2	19.9	295	27	AA819433
	8	29.2	19.9	535	27	AA874935
	9	29.2	19.9	413	27	AA892220
	10	29.2	19.9	454	28	AA801097
	11	29.2	19.9	573	28	AI009661
	12	29.2	19.9	522	30	AI105198
	13	29	19.7	425	19	HSPD06480
C	14	28.8	19.6	579	16	AA204345
	15	28.8	19.6	544	21	AA293284
	16	28.6	19.5	409	14	T15281
C	17	28.4	19.3	484	11	R62406
	18	28.4	19.3	195	12	H81967
C	19	28.4	19.3	412	19	AA400586
	20	28.4	19.3	243	27	H34430
C	21	28.2	19.2	634	14	AA028226
C	22	28.2	19.2	444	14	W42291
C	23	28.2	19.2	619	14	W52157
C	24	28.2	19.2	720	16	AA108435
C	25	28.2	19.2	676	16	AA218243
C	26	28.2	19.2	307	17	AA267667
C	27	28.2	19.2	251	17	AA270488
C	28	28.2	19.2	466	17	AA272879
C	29	28.2	19.2	376	20	AA466633
C	30	28.2	19.2	478	20	AA475090
C	31	28.2	19.2	506	20	AA492778
C	32	28.2	19.2	546	21	AA543228
C	33	28.2	19.2	354	23	AI216242
C	34	28.2	19.2	439	24	AA656473
C	35	28.2	19.2	296	31	AI232782
	36	28	19.0	395	19	HSPD05706
	37	28	19.0	356	21	AA399298
C	38	27.8	18.9	316	11	T29869
	39	27.8	18.9	483	12	N40183
C	40	27.8	18.9	348	14	W37314
	41	27.8	18.9	577	15	AA143783
	42	27.8	18.9	436	23	AI270351
	43	27.8	18.9	400	24	T04238
	44	27.8	18.9	439	26	AA776241
	45	27.8	18.9	764	29	AI052032

ALIGNMENTS

RESULT 1

LOCUS	HSPD04245	443 bp	DNA	EST	21-APR-1997
DEFINITION	H.sapiens EST sequence (011-X4-12) from skeletal muscle, mRNA				
ACCESSION	F19640				
NID	g1136055				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;				
	Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;				
	Homo.				
REFERENCE	1 (bases 1 to 443)				
AUTHORS	Lafranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A., Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G.				
TITLE	Identification of 4,370 expressed sequence tags (ESTs) from a 3'-end specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridisation				
JOURNAL	Genome Res. 1, 35-42 (1996)				
REFERENCE	2 (bases 1 to 443)				
AUTHORS	Valle,G				
TITLE	Direct Submission				
JOURNAL	Submitted (19-DEC-1995) CRIBI Biotechnology Centre, University of Padua, Via Trieste 75, 35121 Padua, Italy				

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Qy 3 ataactggccaacatgactcaagtctcttgaggccaaacaggactcttgatcatcct 62

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Db 203 AGAATTGGCAGCAAGGCTCATGTATACAGAGGCCAGCTGCTCTTCTGCTCTCTCTG 262
Qy 63 gtgggggtgaggtgggacaaaggaaaggggtgaatgtactgtattacaaacctctgg 122
Db 263 TTGGGACAAGGGTGTGAGAAGGTGAGAGGGCATAGCGGACTCTCTCCAGAAAATTTGG 322
Qy 123 tggctgctccccctctgtttatc 146
Db 323 GGGCTCTCTGTCATGTCATCNC 346

RESULT 6
R18712 539 bp mRNA EST 14-APR-1995
LOCUS Yf98f07.r1 Homo sapiens cDNA clone 30551 5' similar to SP:MEC2_RAT
DEFINITION Yf98f07.r1 Homo sapiens cDNA clone 30551 5' similar to SP:MEC2_RAT
ACCESSION R18712
NID 9772322
KEYWORDS EST.
SOURCE human clone-30551 library-Soares infant brain LMB vector-Lafmid BA
host-DHI08 (ampicillin resistant) primer-M13Rp1 Rsite1-Not I
Rsite2-Hind III Whole brain from a 73 days post natal female. 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
ACTGGAAGATTCGGCGCGAGGATTTTCTTTTCTTTT 3']; double-stranded
cDNA was ligated to Hind III adaptors (Pharmacia), digested with
Not I and directionally cloned into the Not I and Hind III sites of
the Lafmid BA vector. Library went through one round of
normalization. Library constructed by Bento Soares and M.Fatima
Bonaldo.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 539)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT GDB: G00-402-898
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 458
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
Location/Qualifiers
1..539
/organism="Homo sapiens"
/clone="30551"
BASE COUNT 140 a 122 c 152 g 116 t 9 others
ORIGIN
Query Match 19.9%; Score 29.2; DB 10; Length 539;
Best Local Similarity 50.8%; Pred. No. 28;
Matches 67; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 1 agtaactgggcaacacatgactcagttctgttggaggcaacagactctgagtcac 60
Db 119 AGAGAAAGAGGGCAAGCATGAGCCGCTGGAGCCATCAGCCACCTCTGCTGAGCCGC 178
Qy 61 ctgtgggggtgggggtgggacaaaggaaaggggtgaatgtactgtattacaaacctct 120
Db 179 AGAGGCAAGGCAAGAGACATCAGAGGGTCAGGCTCCGCCCGGCTGTGGCAANGCT 238

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Qy 121 ggtgctgcctcc 132
Db 239 TCTGCTCCCC 250

RESULT 7
R1819433 295 bp mRNA EST 09-MAR-1998
LOCUS UI-R-A0-bl-h-09-0-UI.s1 UI-R-A0 Rattus norvegicus cDNA clone
DEFINITION UI-R-A0-bl-h-09-0-UI.3' similar to gb|L13257|RATNAP12A Rattus
norvegicus, renal Na/Pi-cotransport mRNA, complete cds, mRNA
sequence.
ACCESSION AA819433
NID 92946932
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 295)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
COMMENT On Mar 10, 1998 this sequence version replaced gi:2889522.
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the
oligo-dT track (not shown) served to identify it as a clone from
the normalized adult kidney library. cDNA library Preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics
Seq primer: M13 Forward.
FEATURES
Location/Qualifiers
1..295
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/note="Vector: pMT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; This library
consists of a mixture of individually tagged normalized
libraries constructed from rat placenta, adult lung,
brain, liver, kidney, heart, spleen, ovary, and muscle.
The tag is a string of 3-5 nucleotides present between the
Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture."
/db_xref="taxon:10116"
/clone="UI-R-A0-bl-h-09-0-UI"
/clone_lib="UI-R-A0"
/dev_stage="adult"
/lab_host="DHI08 (Life Technologies)"
BASE COUNT 75 a 76 c 68 g 76 t
ORIGIN
Query Match 19.9%; Score 29.2; DB 27; Length 295;
Best Local Similarity 50.7%; Pred. No. 27;
Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 3 ataactggcaccactgactcagttctgttgaggccaaacagactctgagtcacct 62
Db 47 AGAATTGGCAGCAAGGCTCATGTATACAGAGGCCAGCTCTCTTCTGCTCTCTG 106
Qy 63 gtgggggtgaggtgggacaaaggaaaggggtgaatgtactgtattacaaacctctg 122
Db 107 TTGGCAAGGGTAGTGAGAAGGTGAGAGGGCATAGCGGACTCTCTCCAGAAAATTTGG 166

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Qy 123 tgcgtcctccccctctg 140
Db 167 GGGCTCCTCATGCATCTG 184

RESULT 8
AA874935 535 bp mRNA EST 20-MAR-1998
LOCUS UI-R-E0-ci-c-06-0-UI.s1 UI-R-E0 Rattus norvegicus cDNA clone
DEFINITION UI-R-E0-ci-c-06-0-UI 3' similar to gi1816434|dbj|AB000733|AB000733
ACCESSION AB874935
NID 92979883
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
AUTHORS Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 535)
TITLE Bonaldo,M.F., Lennon,G. and Soares,M.B.
JOURNAL Normalization and subtraction: two approaches to facilitate gene
MEDLINE discovery
COMMENT Genome Res. 6 (9), 791-806 (1996)
97044477

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

The sequence tag present in the cDNA between the NotI site and the
oligo-dT track (not shown) served to identify it as a clone from
the normalized adult 12-day-Embryo library. CDNA Library
Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones
will be available through Research Genetics
Seq primer: M13 Forward.

FEATURES
Location/Qualifiers
source 1..535
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/vector="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: NotI; Site_2: EcoRI; This library
consists of a mixture of individually tagged normalized
libraries constructed from 8, 12 and 18-day embryo. The
tag is a string of 3-5 nucleotides present between the
Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture."
/db_xref="taxon:10116"
/clone="UI-R-E0-ci-c-06-0-UI"
/clone_lib="UI-R-E0"
/dev_stage="embryonic"
/lab_host="DH10B (Life Technologies)"

BASE COUNT 156 a 123 c 113 g 143 t
ORIGIN

Query Match 19.9%; Score 29.2; DB 27; Length 535;
Best Local Similarity 59.8%; Pred. No. 28;
Matches 49; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 49 ttctgagtcacctgtgggggtggaggggacagggggaaggggtgaatggtactgctg 108
Db 46 TTCAGCGCAATAGCTTTGGAGGAATGGGACAGGGGTAGGGTCTCAATGTAATGCTT 105

Qy 109 attacaacctctgtgtgctc 130
Db 106 ATTTCAGGTCCTTATGTAGCT 127

us-09-205-015-2.rst

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RESULT 9
AA892220 413 bp mRNA EST 03-APR-1998
LOCUS EST196023 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
DEFINITION RKIAN83 3' end, mRNA sequence.
ACCESSION AA892220
NID 93019099
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
AUTHORS Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 413)
TITLE Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
JOURNAL Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
MEDLINE Gene Index
COMMENT Unpublished (1998)

Contact: Lee, NH
ATCC
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.

FEATURES
Location/Qualifiers
source 1..413
/organism="Rattus sp."
/clone="Organ: kidney; Vector: pT73Pac; Site_1: EcoRI;
Site_2: NotI"
/db_xref="taxon:10118"
/clone="RKIAN83"
/clone_lib="Normalized rat kidney, Bento Soares"

BASE COUNT 111 a 112 c 93 g 97 t
ORIGIN

Query Match 19.9%; Score 29.2; DB 27; Length 413;
Best Local Similarity 50.7%; Pred. No. 27;
Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 3 ataactggggcacaaccatgactcagtcgtctgtggagggcacaaggagctctgagtcactc 62
Db 48 AGAATTGGCAGAGGAAGGCTCATGTATACAGAGAGCCAGCTGCTCTCTGCGCTCTCTG 107

Qy 63 gtgggggtgagggtgggacagggaagggtgaatggtgactgctgattacaacctg 122
Db 108 TTGGACAAGGGTATGAGAGAGGTGAGAGGGCATAGCGGACTCTCCAGAAAATTTGG 167

Qy 123 tgcgtcctccccctctg 140
Db 168 GGGCTCCTCATGCATCTG 185

RESULT 10
AA801097 454 bp mRNA EST 30-APR-1998
LOCUS EST190594 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
DEFINITION ROVAAS4 3' end, mRNA sequence.
ACCESSION AA801097
NID 92864052
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
AUTHORS Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 454)
TITLE Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
JOURNAL Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
MEDLINE Gene Index

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RESULT 13
HSPD06480

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LOCUS       HSPD06480      425 bp      DNA      EST      30-APR-1997
DEFINITION   H.sapiens EST sequence (081-X1-15) from skeletal muscle, mRNA
ACCESSION   F21884
NID         G2061060
KEYWORDS     EST..
SOURCE      Homo sapiens
ORGANISM     Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
             Homo.
REFERENCE    1 (bases 1 to 425)
AUTHORS     Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A.,
             Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G.
TITLE       Identification of 4,370 expressed sequence tags (ESTs) from a
             3'-end specific cDNA library of human skeletal muscle by DNA
             sequencing and filter hybridisation
JOURNAL     Genome Res. 1, 35-42 (1996)
REFERENCE    2 (bases 1 to 425)
AUTHORS     Valle,G.
TITLE       Direct Submission
JOURNAL     Submitted (29-APR-1997) CRIBI Biotechnology Centre, University of
             Padua, Via U. Bassi 58/B, 35121 Padua, Italy
COMMENT     ABI Chromatograms and other information are available on WWW at
             http://eos.bio.unipd.it
             V_type: Plasmid
             Vector: pCDNAII (Invitrogen)
             RE_1: BstXI
             RE_2: NotI
             PRIMER: PC2R
DESCR:      The library was constructed by G. Lanfranchi. This library
             is not subtracted nor normalized. The first strand cDNA was primed
             with a biotinylated oligo-dT-NotI primer
             (5'-biotin-AACCGCTGAGCGCGCTTTT-3'). The ds cDNA
             was sonicated and size-selected in the range 350-550 bp.
             The 3' specific fragments were selected by streptavidin coated
             magnetic beads, ligated to non-palindromic BstXI adapters, NotI
             digested and directionally cloned into BstXI-NotI cut pCDNAII
             vector.
FEATURES             Location/Qualifiers
             1..425
             /organism="Homo sapiens"
             /note="caucasian"
             /db_xref="taxon:9606"
             /tissue_type="pectoral muscle (after mastectomy)"
             /clone_lib="HM3"
             /sex="female"
BASE COUNT      90 a 143 c 88 g 102 t 2 others
ORIGIN
Query Match      19.7%; Score 29; DB 19; Length 425;
Best Local Similarity 57.5%; Pred.No.31;
Matches 50; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 35 gagggcaacagactcttgatcctctgtgggtgggtggaggtgggacaggaagggt 94
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 269 GAAGCACTGGGGCTCTCAGCCACCCCTGCTGTACAAAGTGGAAGAGAGAGGGGT 328
QY 95 gaatggactgtgtattacaacctgtg 121
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 329 GAAACACCTTCTCTCCANCCCTGTG 355

RESULT 14
AA204345/c
LOCUS         AA204345      579 bp      mRNA      EST      19-FEB-1997
DEFINITION   mu31b06.r1 Soares 2NbMT Mus musculus cDNA clone 640979 5', mRNA
ACCESSION   AA204345
NID         91800942
KEYWORDS     EST.
SOURCE      house mouse.

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ORGANISM      Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
REFERENCE    1 (bases 1 to 579)
AUTHORS     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
             Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
             Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
             Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
             Waterston,R.
TITLE       The WashU-HMI Mouse EST Project
JOURNAL     Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
             WashU-HMI Mouse EST Project
             Washington University School of Medicine
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: mouseest@watson.wustl.edu
             This clone is available royalty-free through LLNL; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
             MGI:392971
             Seq primer: -28M13 rev2 from Amersham
             High quality sequence stop: 495.
FEATURES             Location/Qualifiers
             1..579
             /organism="Mus musculus"
             /strain="C57BL/6J"
             /note="Vector: pT73D-Pac (Pharmacia) with a modified
             polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
             was primed with a Not I - oligo(dT) primer [5',
             TGTTACCAATCTGAAGTGGAGCGCGCTTTT-3']; double-stranded cDNA was ligated to Eco RI adapters
             (Pharmacia), digested with Not I and cloned into the Not I
             and Eco RI sites of the modified pT73 vector. RNA
             provided by Dr. Bertrand Jordan. Library went through two
             rounds of normalization, and was constructed by Bento
             Soares and M.Fatima Bonaldo."
             /db_xref="taxon:10090"
             /clone_lib="Soares 2NbMT"
             /sex="male"
             /tissue_type="Thymus"
             /dev_stage="4 weeks"
             /lab_host="DH10B"
BASE COUNT      142 a 170 c 135 g 131 t 1 others
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Query Match      19.6%; Score 28.8; DB 16; Length 579;
Best Local Similarity 61.6%; Pred.No.36;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 63 gtgggggtggaggtgggacagggaagggtgaaagtgtactgtctgattacaacctgtg 122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 255 GTGGGGTGGGGATGGTGGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 196
QY 123 tgtgtcctcccc 135
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 195 TGCTGCTGCACCC 183

RESULT 15
AA293284
LOCUS         AA293284      544 bp      mRNA      EST      12-AUG-1997
DEFINITION   zt55e11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 726284
             5', similar to gb:223090 HEAT SHOCK 27 KD PROTEIN (HUMAN);, mRNA
             sequence.
ACCESSION   AA293284
NID         91941566
KEYWORDS     EST.

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SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
Homo.

REFERENCE 1 (bases 1 to 544)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
TITLE WashU-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 617 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 166.
Location/Qualifiers
1. .544
/organism="Homo sapiens"
/note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site1: Not I; Site2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(df) primer [5'
TGTACCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone="726284"
/clone_lib="Soares ovary tumor NBHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/cl. .>544
/db_xref="GDB:5938368"
BASE COUNT 114 a 190 c 143 g 96 t 1 others
ORIGIN

Query Match 19.68; Score 28.8; DB 21; Length 544;
Best Local Similarity 55.7%; Pred. No. 36;
Matches 54; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 51 ctgagtcacgtctgggggtggaggtgggacagggaagggtgaatgtactgtgat 110
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 400 CTGCAAAATCCGATGAGACTGGCGCAAGTAAGCCCTTATGCCCGGATGCCACCCCTGCT 459
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 111 tacacacctctgtgctgctccctccctctcttctatct 147
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 460 TGCCGCCACCTGGCTGTGCTCTCCCGCGCACACGTGTGT 496
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Search completed: June 23, 1999, 23:01:47
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